

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

1.-8. (canceled)

9. (currently amended) The method of any one of claims 11 or 12 [[1-4]], wherein said sample is a drop of blood.

10. (currently amended) The method of any one of claims 11 or 12 [[1-4]], wherein said blood sample is from a human.

11. (New) A method of identifying two or more genes differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types from subjects having a disease as compared with subjects not having said disease, said method comprising:

for each gene of a collection of two or more genes:

(a) using an oligonucleotide of predetermined sequence, detecting an amount of an RNA encoded by said gene in total blood cell RNA of blood samples which have not been fractionated into cell types from subjects having said disease, said oligonucleotide being specific only for said RNA, or cDNA complementary to said RNA, encoded by said gene in said samples, said gene being expressed in blood and in a heart tissue of a subject not having said disease;

(b) quantifying said amount of said RNA encoded by said gene in total blood cell RNA of said blood samples; and

(c) determining a difference between said quantified amount and a quantified amount of said RNA encoded by said gene in total blood cell RNA of control blood samples which have not been fractionated into cell types from control subjects, said RNA having been detected in said samples from said control subjects,

thereby identifying each of said two or more genes as being differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types as between subjects having a disease and subjects not having said disease.

12. (New) A method of identifying two or more genes differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types from subjects having a disease as compared with subjects not having said disease, said method comprising:

for each gene of a collection of two or more genes:

(a) producing amplification products from an RNA encoded by said gene from total blood cell RNA of blood samples which have not been fractionated into cell types from subjects having said disease, using primers specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene in said samples, said gene being expressed in blood and in heart tissue of a subject not having said disease;

(b) quantifying said amplification products of said RNA encoded by said gene in total blood cell RNA of said blood samples; and

(c) determining a difference between said quantity of said amplification products and a quantity of amplification products from RNA encoded by said gene from total blood cell RNA of control blood samples which have not been fractionated into cell types from control subjects, said amplification products of said control samples having been detected in said samples using primers specific only for said RNA, and/or cDNA complementary to said RNA, encoded by said gene;

thereby identifying said two or more genes as being differentially expressed in total blood cell RNA of blood samples which have not been fractionated into cell types from subjects having a disease as compared with subjects not having said disease.